

REMARKS

1. Preliminary Remarks

a. Status of the Claims

Claims 21-31 were pending in this application. In order to expedite prosecution and without prejudice to Applicant's right to pursue the canceled subject matter in a continuing application, Applicant hereby cancels claims 30 and 31, and amends claims 21, 23, and 27. Upon entry of these amendments pursuant to 37 C.F.R. § 1.111, claims 21-29 are pending and under active consideration. Applicants respectfully request entry of the amendments and remarks made herein into the file history of the present application.

b. Amendments to the Claims

Claim 21 is amended to recite that the sequence of the nucleic acid comprises: (a) at least 18 consecutive nucleotides of SEQ ID NO: 863, support for which can be found at SEQ ID NO: 863 and claim 1 as originally filed.

Claim 21 is also amended to recite that the nucleic acid comprises: (c) a sequence at least 71.3% identical to (a) or (b), support for which can be found at claim 1 and at Table 1 as originally filed. SEQ ID NO: 863 forms a hairpin, as shown at Table 1. SEQ ID NO: 863 is 87 nucleotides in length. Within the predicted hairpin formed by SEQ ID NO: 863, 62 complementary nucleotides are paired. The ratio 62/87 expressed as a percent, rounded up to the nearest tenth, is equivalent to 71.3%.

Claim 23 is amended to recite a nucleic acid with a sequence consisting of: (a) SEQ ID NO: 863, support for which can be found at claim 23 as previously presented. Claim 23 is also amended to recite that the sequence of the nucleic acid consists of: (c) a sequence at least 71.3% nucleotides identical to (a) or (b), support for which can be found as described for claim 21 above.

Claim 27 is amended to recite the nucleic acid of claim 26, wherein the nucleic acid is at least 71.5% complementary to a binding site sequence, support for which can be found at claim 1 and at Table 2 as originally filed. Table 2 shows that among all listed target binding sites for the nucleotide sequence represented by SEQ ID NO: 3588, 15 nucleotides of a 21 nucleotide target binding site (15/21) is the lowest level of complementarity found between SEQ ID NO: 3588 and

a target binding site.¹ Accordingly, the percent equivalent of the ratio 15/21, rounded up to the nearest tenth, is 71.5%.

c. Amendments to the Specification

The title of the application is amended to strike the word “novel,” support for which can be found at the title of the application as originally filed.

Paragraph 0052 is amended to assign SEQ ID NO: 46756 to the sequence shown in Fig. 12A in compliance with 37 C.F.R. §§ 1.821-1.825.

Paragraph 0055 is amended to assign SEQ ID NO: 46756 to the sequence shown in Fig. 13A in compliance with 37 C.F.R. §§ 1.821-1.825.

Paragraph 0058 is amended to assign SEQ ID NO: 46758 to the sequence shown in Fig. 14A in compliance with 37 C.F.R. §§ 1.821-1.825.

Paragraph 0150 is amended to assign SEQ ID NOS: 46759-46764 to the listed sequences in compliance with 37 C.F.R. §§ 1.821-1.825. Paragraph 0150 is also amended to correct typographical errors.

The abstract is amended to strike the term “novel,” support for which can be found at the abstract as originally filed.

2. Objections to the Specification

a. Sequence Rule Compliance

On pages 2 and 4 of the Office Action, the Examiner objects to the sequence disclosures in the specification for allegedly failing to comply with 37 C.F.R. §§ 1.821-1.825. Specifically, the Examiner alleges that SEQ ID NO identifiers are not associated with Figures 12A, 13A, 14A and paragraph 0150.

Applicant hereby amends paragraphs 0052, 0055, and 0058 to assign SEQ ID NOS: 46756, 46757, and 46758, respectively, to the sequences shown in Figures 12A, 13A, and 14A. Applicant further amends paragraph 0150 to assign SEQ ID NOS: 46759-46764 to the listed sequences.

Applicant submits that the sequences disclosed in the above-mentioned amended paragraphs comply with 37 C.F.R. §§ 1.821-1.825. In view of the foregoing amendments,

¹ The nucleotide sequence of SEQ ID NO: 3588 is a part within the nucleotide set forth in SEQ ID NO: 863.

Applicant respectfully submits that the objection to the sequence disclosures has been overcome and requests that the objection be reconsidered and withdrawn.

b. Title and Abstract

On page 4 of the Office Action, the Examiner objects to the specification for containing the term novel because this term is allegedly not descriptive of the claimed subject matter. Applicant hereby amends the title and abstract of the application to strike the word “novel.” In view of the foregoing amendments, Applicant submits that the objection to the specification has been overcome and respectfully requests that the objection be reconsidered and withdrawn.

3. Claim Objections

On page 4 of the Office Action, the Examiner objects to claims 21-23 for allegedly containing non-elected subject matter.

Amended claims 21 and 23 are no longer directed to the non-elected SEQ ID NOS: 861 or 862. Claim 22 recites SEQ ID NO: 3588, which is a sequence consisting of nucleotides 53-76 of SEQ ID NO: 863. In other words, SEQ ID NO: 3588 is a nucleic acid sequence of “18 to 120 nucleotides” of SEQ ID NO: 863, which has been searched by the Examiner. Therefore, SEQ ID NO: 3588 would not require a separate search. Accordingly, Applicant respectfully submits that claims 21-23 are directed to the elected claimed subject matter consistent with Applicant’s reply of August 16, 2006. In view of the foregoing amendments and remarks, Applicant respectfully submits that the objections to claims 21-23 have been overcome and requests that the objections be reconsidered and withdrawn.

4. Patentability Remarks

a. Rejection Pursuant to 35 U.S.C. § 112, Second Paragraph

Claims 21-31

On page 5 of the Office Action, the Examiner rejects claims 21-31 under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite. Specifically, the Examiner alleges that the ratio 62/87 of claim 21 and the ratio of 15/21 of claim 27 are not defined by the specification and indicate ratios between two different oligonucleotides. Applicant respectfully disagrees. Applicant respectfully submits that the terms 62/87 and 15/21 are defined by the number of complementary bases in either a hairpin or between a nucleic acid, such as a miRNA, and a target nucleic acid. Specifically, the ratio 62/87 refers to the number of complementary bases in a hairpin stem over the length of the predicted hairpin nucleotide sequence as set forth in SEQ ID

NO: 863. The predicted hairpin of SEQ ID NO: 863 is shown in Table 1. The ratio 15/21 refers to the lowest number of complementary bases between SEQ ID NO: 3588 and a target binding site of 21 bases as shown in Table 2. Accordingly, the ratio of base complementarity within the hairpins of Table 1 or between SEQ ID NO: 3588 and a target nucleotide binding sequence of Table 2 are distinct subject matter that can be identified by one of skill in the art.

Nevertheless, in order to expedite prosecution, part (c) of claims 21 and 23 are amended to recite a percent identity, rounded up to the nearest tenth, that is equivalent to the disclosed ratios. Specifically, part (c) of claims 21 and 23 is directed to a sequence that is at least 71.3% identical to (a) or (b). As amended, the ratio 62/87 is now expressed as a percent, rounded up to the nearest tenth, which is equivalent to 71.3%.

Additionally, claim 27 is amended to recite, in part, a nucleic acid “at least 71.5% complementary to a binding site sequence of 18 to 24 nucleotides.” As amended the ratio 15/21 is now expressed as a percent, rounded up to the nearest tenth, which is equivalent to 71.5%.

In view of the foregoing, Applicant respectfully submits that one of skill in the art would be able to easily identify the specific subject matter of variance from the percent base complementarity required of the hairpin sequences of Table 1 or between SEQ ID NO: 3588 and a target nucleotide binding site of Table 2. Accordingly, Applicant respectfully submits that the percent identities in amended claims 21 and 23 are supported by the specification and are definite.

In view of the foregoing remarks and amendments, Applicant respectfully submits that the rejection of claims 21-31 under 35 U.S.C. § 112, second paragraph, for allegedly being indefinite, is overcome and requests that the rejection be reconsidered and withdrawn.

Claim 23

At page 5 of the Office Action, the Examiner alleges that claim 23 is internally inconsistent because it is unclear and ambiguous how SEQ ID NO: 863 consisting of 87 nucleotides can consist of an isolated nucleic acid consisting of 18 to 120 nucleotides. Applicant respectfully disagrees. The Examiner has mistakenly misread the order of the phrases in connection with the terms “consists of.” It is the “isolated nucleic acid consisting of 18 to 120 nucleotides” that is “consisting of 87 nucleotides.” Nevertheless, in order to advance prosecution, claim 23 is amended to no longer recite the length limitation of 18 to 120 nucleotides. In view of the

foregoing amendment, Applicant respectfully requests that the rejection of claim 23 is overcome and requests that the rejection be reconsidered and withdrawn.

b. Rejection Pursuant to 35 U.S.C. § 112, First Paragraph, Enablement

Claims 30-31

At page 6 of the Office Action, the Examiner rejects claims 30-31 under 35 U.S.C. § 112, first paragraph. As discussed above, claims 30 and 31 are canceled without prejudice, rendering the rejection moot.

5. Conclusion

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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